

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/822,186DATE: 06/16/97  
TIME: 18:18:32

INPUT SET: S18376.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

ENTERED

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: RUEGER, David C.  
6 TUCKER, Marjorie M.  
7  
8 (ii) TITLE OF INVENTION: IMPROVED OSTEOGENIC DEVICES AND METHODS  
9 OF USE THEREOF FOR REPAIR OF ENDOCHONDRAL BONE AND  
10 OSTEOCHONDRAL DEFECTS  
11  
12 (iii) NUMBER OF SEQUENCES: 9  
13  
14 (iv) CORRESPONDENCE ADDRESS:  
15 (A) ADDRESSEE: CREATIVE BIOMOLECULES, INC  
16 (B) STREET: 45 SOUTH STREET  
17 (C) CITY: HOPKINTON  
18 (D) STATE: MA  
19 (E) COUNTRY: USA  
20 (F) ZIP: 01748  
21  
22 (v) COMPUTER READABLE FORM:  
23 (A) MEDIUM TYPE: Floppy disk  
24 (B) COMPUTER: IBM PC compatible  
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
27  
28 (vi) CURRENT APPLICATION DATA:  
29 (A) APPLICATION NUMBER:  
30 (B) FILING DATE:  
31 (C) CLASSIFICATION:  
32  
33 (viii) ATTORNEY/AGENT INFORMATION:  
34 (A) NAME: VITO, CHRISTINE C  
35 (B) REGISTRATION NUMBER: 39,061  
36 (C) REFERENCE/DOCKET NUMBER: CRP-137  
37  
38 (ix) TELECOMMUNICATION INFORMATION:  
39 (A) TELEPHONE: (617) 248-7000  
40 (B) TELEFAX: (617) 248-7100  
41  
42  
43 (2) INFORMATION FOR SEQ ID NO:1:  
44  
45 (i) SEQUENCE CHARACTERISTICS:  
46 (A) LENGTH: 1822 base pairs

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47      (B) TYPE: nucleic acid
48      (C) STRANDEDNESS: single
49      (D) TOPOLOGY: linear
50
51      (ii) MOLECULE TYPE: cDNA
52
53      (vi) ORIGINAL SOURCE:
54          (A) ORGANISM: HOMO SAPIENS
55          (F) TISSUE TYPE: HIPPOCAMPUS
56
57      (ix) FEATURE:
58          (A) NAME/KEY: CDS
59          (B) LOCATION: 49..1341
60          (C) IDENTIFICATION METHOD: experimental
61          (D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
62      /product= "OP1"
63      /evidence= EXPERIMENTAL
64      /standard_name= "OP1"
65
66
67      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
68
69      GGTGCGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG      57
70                                          Met His Val
71                                          1
72
73      CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA      105
74      Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
75          5              10              15
76
77      CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC      153
78      Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
79          20              25              30              35
80
81      GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG      201
82      Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
83          40              45              50
84
85      CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC      249
86      Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
87          55              60              65
88
89      CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG      297
90      Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
91          70              75              80
92
93      CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC      345
94      Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
95          85              90              95
96
97      GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC      393
98      Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
99      100              105              110              115

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100																	
101	CCC	CCT	CTG	GCC	AGC	CTG	CAA	GAT	AGC	CAT	TTC	CTC	ACC	GAC	GCC	GAC	441
102	Pro	Pro	Leu	Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	Asp	Ala	Asp	
103					120				125						130		
104																	
105	ATG	GTC	ATG	AGC	TTC	GTC	AAC	CTC	GTG	GAA	CAT	GAC	AAG	GAA	TTC	TTC	489
106	Met	Val	Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	Glu	Phe	Phe	
107				135				140					145				
108																	
109	CAC	CCA	CGC	TAC	CAC	CAT	CGA	GAG	TTC	CGG	TTT	GAT	CTT	TCC	AAG	ATC	537
110	His	Pro	Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile	
111			150					155					160				
112																	
113	CCA	GAA	GGG	GAA	GCT	GTC	ACG	GCA	GCC	GAA	TTC	CGG	ATC	TAC	AAG	GAC	585
114	Pro	Glu	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp	
115		165					170					175					
116																	
117	TAC	ATC	CGG	GAA	CGC	TTC	GAC	AAT	GAG	ACG	TTC	CGG	ATC	AGC	GTT	TAT	633
118	Tyr	Ile	Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Arg	Ile	Ser	Val	Tyr	
119	180					185					190					195	
120																	
121	CAG	GTG	CTC	CAG	GAG	CAC	TTG	GGC	AGG	GAA	TCG	GAT	CTC	TTC	CTG	CTC	681
122	Gln	Val	Leu	Gln	Glu	His	Leu	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu	
123					200				205						210		
124																	
125	GAC	AGC	CGT	ACC	CTC	TGG	GCC	TCG	GAG	GAG	GGC	TGG	CTG	GTG	TTT	GAC	729
126	Asp	Ser	Arg	Thr	Leu	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp	
127				215				220					225				
128																	
129	ATC	ACA	GCC	ACC	AGC	AAC	CAC	TGG	GTG	GTC	AAT	CCG	CGG	CAC	AAC	CTG	777
130	Ile	Thr	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu	
131			230					235					240				
132																	
133	GGC	CTG	CAG	CTC	TCG	GTG	GAG	ACG	CTG	GAT	GGG	CAG	AGC	ATC	AAC	CCC	825
134	Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro	
135		245					250					255					
136																	
137	AAG	TTG	GCG	GGC	CTG	ATT	GGG	CGG	CAC	GGG	CCC	CAG	AAC	AAG	CAG	CCC	873
138	Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro	
139	260																

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153	AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC	1065
154	Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe	
155	325 330 335	
156		
157	CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC	1113
158	Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala	
159	340 345 350 355	
160		
161	GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG	1161
162	Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met	
163	360 365 370	
164		
165	AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC	1209
166	Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn	
167	375 380 385	
168		
169	CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC	1257
170	Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala	
171	390 395 400	
172		
173	ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA	1305
174	Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys	
175	405 410 415	
176		
177	TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC	1351
178	Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His	
179	420 425 430	
180		
181	GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG	1411
182		
183	GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG	1471
184		
185	TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTTT CAGTGGCAGC	1531
186		
187	ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAACAAC	1591
188		
189	GCATAAAGAA AAATGGCCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT	1651
190		
191	CGTTTCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG	1711
192		
193	GGCGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC	1771
194		
195	CTGTAATAAAA TGTCAACAATA AAACGAATGA ATGAAAAAAA AAAAAAAAAA A	1822
196		
197		
198	(2) INFORMATION FOR SEQ ID NO:2:	
199		
200	(i) SEQUENCE CHARACTERISTICS:	
201	(A) LENGTH: 431 amino acids	
202	(B) TYPE: amino acid	
203	(D) TOPOLOGY: linear	
204		
205	(ii) MOLECULE TYPE: protein	

RAW SEQUENCE LISTING  
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206  
207 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
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209 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala  
210 1 5 10 15  
211  
212 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser  
213 20 25 30  
214  
215 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser  
216 35 40 45  
217  
218 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu  
219 50 55 60  
220  
221 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro  
222 65 70 75 80  
223  
224 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly  
225 85 90 95  
226  
227 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser  
228 100 105 110  
229  
230 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr  
231 115 120 125  
232  
233 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys  
234 130 135 140  
235  
236 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu  
237 145 150 155 160  
238  
239 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile  
240 165 170 175  
241  
242 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile  
243 180 185 190  
244  
245 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu  
246 195 200 205  
247  
248 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu  
249 210 215 220  
250  
251 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg  
252 225 230 235 240  
253  
254 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser  
255 245 250 255  
256  
257 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn  
258 260 265 270

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**SEQUENCE VERIFICATION REPORT**  
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*INPUT SET: S18376.raw*

Line

Error

Original Text

